

1600

RAW SEQUENCE LISTING DATE: 03/29/2004 DATE: 03/29/2004 DATE: 09:56:27

Input Set : A:\3-19-04 KATO revised sequence listing.txt

```
5 <110> APPLICANT: Seishi KATO
             Tomoko KIMURA
      9 <120> TITLE OF INVENTION: Human proteins having hydrophobic domains and DNAs encoding
these
             proteins
     14 <130> FILE REFERENCE: 2003-0986/WMC/01791
     17 <140> CURRENT APPLICATION NUMBER: 10/019,114A
C--> 18 <141> CURRENT FILING DATE: 2001-12-21
     21 <150> PRIOR APPLICATION NUMBER: JP 11-188835
                                                               ENTERED
     22 <151> PRIOR FILING DATE: 1999-07-02
     25 <160> NUMBER OF SEQ ID NOS: 30
     28 <210> SEQ ID NO: 1
     29 <211> LENGTH: 233
     30 <212> TYPE: PRT
     31 <213> ORGANISM: Homo sapiens
     35 <400> SEQUENCE: 1
     37 Met Trp Gln Leu Leu Ala Ala Cys Trp Met Leu Leu Leu Gly Ser
                          5
     41 Met Tyr Gly Tyr Asp Lys Lys Gly Asn Asn Ala Asn Pro Glu Ala Asn
                     20
     45 Met Asn Ile Ser Gln Ile Ile Ser Tyr Trp Gly Tyr Pro Tyr Glu Glu
     47
     49 Tyr Asp Val Thr Thr Lys Asp Gly Tyr Ile Leu Gly Ile Tyr Arg Ile
                                 55
     53 Pro His Gly Arg Gly Cys Pro Gly Arg Thr Ala Pro Lys Pro Ala Val
     57 Tyr Leu Gln His Gly Leu Ile Ala Ser Ala Ser Asn Trp Ile Cys Asn
                         85
                                             90
     61 Leu Pro Asn Asn Ser Leu Ala Phe Leu Leu Ala Asp Ser Gly Tyr Asp
                   100
                                        105
                                                            110
     65 Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Leu
                                    120
                                                        125
     69 Lys Leu Ser Pro Lys Ser Pro Glu Tyr Trp Ala Phe Ser Leu Asp Glu
                                135
     73 Met Ala Lys Tyr Asp Leu Pro Ala Thr Ile Asn Phe Ile Ile Glu Lys
                            150
                                                                    160
     77 Thr Gly Gln Lys Arg Leu Tyr Tyr Val Gly His Ser Gln Gly Thr Thr
    79
                        165
                                            170
    81 Ile Ala Phe Ile Ala Phe Ser Thr Asn Pro Glu Leu Ala Lys Lys Ile
                                        185
    85 Lys Ile Phe Phe Ala Leu Ala Pro Val Val Thr Val Lys Tyr Thr Gln
                                    200
               195
                                                        205
    89 Ser Pro Met Lys Lys Leu Thr Thr Leu Ser Arg Arg Val Val Lys Val
                                215
                                                    220
            210
```

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93 Cys Asp Phe Pro Ser Phe Asn Leu Lys
95 225
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 273
100 <212> TYPE: PRT
101 <213> ORGANISM: Homo sapiens
103 <400> SEQUENCE: 2
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109 Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val Cys Ala
                20 .
113 Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val Gln Arg Val
            35
                                 40
117 Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg Ala Cys Ser Thr
121 Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg Ser Pro Gly Leu Ala
125 Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro Gly Trp Lys Arg Thr Ser
127
129 Gly Leu Pro Gly Ala Cys Gly Ala Ala Ile Cys Gln Pro Pro Cys Arg
                                    105
133 Asn Gly Gly Ser Cys Val Gln Pro Gly Arg Cys Arg Cys Pro Ala Gly
           115
                                 120
                                                    125
137 Trp Arg Gly Asp Thr Cys Gln Ser Asp Val Asp Glu Cys Ser Ala Arg
                            135
141 Arg Gly Gly Cys Pro Gln Arg Cys Val Asn Thr Ala Gly Ser Tyr Trp
                        150
                                            155
145 Cys Gln Cys Trp Glu Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys
                    165
                                        170
149 Val Pro Lys Gly Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val
                180
                                    185
153 Asp Ser Ala Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp
                                200
157 Leu Leu Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu
        210
                            215
                                                220
161 Ala Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu
                        230
                                            235
165 Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu Gln
                                        250
                    245
169 Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys Lys Asp
171
                260
                                    265
173 Ser
175 <210> SEQ ID NO: 3
176 <211> LENGTH: 282
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 3
182 Met Ser Gly Ser Ser Leu Pro Ser Ala Leu Ala Leu Ser Leu Leu Leu
184
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186 188	Val	Ser	Gly	Ser 20	Leu	Leu	Pro	Gly	Pro 25	Gly	Ala	Ala	Gln	Asn 30	Glu	Pro
190 192	Arg	Ile	Val 35	Thr	Ser	Glu	Glu	Val 40	Ile	Ile	Arg	Asp	Ser 45	Pro	Val	Leu
194 196	Pro	Val 50	Thr	Leu	Gln	Cys	Asn 55	Leu	Thr	Ser	Ser	Ser 60	His	Thr	Leu	Thr
198 200	Tyr 65	Ser	Tyr	Trp	Thr	Lys 70	Asn	Gly	Val	Glu	Leu 75	Ser	Ala	Thr	Arg	Lys 80.
202 204	Asn	Àla	Ser	Asn	Met 85		Tyr	Arg	Ile	Asn 90	Lys	Pro	Arg	Ala	Glu 95	Asp
206 208	Ser	Gly	Glu	Tyr 100	His	Cys	Val	Tyr	His 105	Phe	Val	Ser	Ala	Pro 110	Lys	Ala
210 212	Asn	Ala	Thr 115	Ile	Glu	Val	Lys	Ala 120	Ala	Pro	Asp	Ile	Thr 125	Gly	His	Lys
214 216	_	Ser 130	Glu	Asn	Lys	Asn	Glu 135	Gly	Gln	Asp	Ala	Thr 140	Met	Tyr	Cys	Lys
220	145		Gly			150					155				:	160
224	_		Pro		165					170	_	_			175	
228		_	Glu	180					185					190		
232		_	Pro 195	_		-		200					205			
236		210	Val	•			215	_				220				
240	225		Phe		_	230					235					240
244			Val		245	_		_	_	250	_				255	
248	_		Pro	260	-			_	265		Ser	Thr	Asn	270	HIS	ьуs
252	_	_	Asn 275		_	GIn	Arg	280	Tnr.	Asn					•	
			EQ II													
			ENGTI YPE:		30								•			
			RGAN:		Ното	sar	oi ens	3								•
			EQUE			, Du		•								
			Leu			His	Ser	Met	Gln	Ala	Leu	Ser	Trp	Ara	Lvs	Leu
264	1				5					10			•	,	15	•
266 268	Tyr	Leu	Ser	Arg 20	Ala	Lys	Leu	Lys	Ala 25	Ser	Ser	Arg	Thr	Ser 30	Ala	Leu
270 272	Leu	Ser	Gly 35	Phe	Ala	Met	Val	Ala 40	Met	Val	Glu	Val	Gln 45	Leu	Asp	Ala
274 276	Asp	His 50	Asp	Tyr	Pro	Pro	Gly 55	Leu	Leu	Ile	Ala	Phe 60	Ser	Ala	Cys	Thr
278 280	Thr 65	Val	Leu	Val	Ala	Val 70	His	Leu	Phe	Ala	Leu 75	Met	Ile	Ser	Thr	Cys 80

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282 284	Ile	Leu	Pro	Asn		Glu	Ala	Val	Ser		Val	His	Asn	Leu		Ser	
	Val	T.ve	Glu	Ser	85 Pro	His	Glu	Ara	Mot	90 His	Δra	His	Tle	Glu	95 T.e.i	Δla	
288	Vai	цуз	Gru	100	110	1113	OIU	nra	105	1113	Arg	1113	110	110	пси	mu	
	Trp	Ala	Phe		Thr	Val	Ile	Glv		Leu	Leu	Phe	Leu		Glu	Val	
292			115	-				120					125				
	Val	Leu	Leu	Cys	Trp	Val	Lys	Phe	Leu	Pro	Leu	Lys	Lys	Gln	Pro	Gly	
296		130		-	-		135					140	_				
298	Gln	Pro	Arg	Pro	Thr	Ser	Lys	Pro	Pro	Ala	Ser	Gly	Ala	Ala	Ala	Asn	
	145					150					155					160	
	Val	Ser	Thr	Ser		Ile	Thr	Pro	Gly		Ala	Ala	Ala	Ile		Ser	
304	m)	m)	~ 1		165		D1.	6 1	_	170	731	- 1	** - 7	51	175	** - 7	
	Thr	Thr	тте	Met 180	vaı	Pro	Pne	GTÀ	ьеи 185	тте	Phe	тте	vaı	190	Ата	vaı	
308	uic	Pho	ጥ፣፣ም	Arg	Sor	Lon	Wal	Sar		Tue	Thr	Acn	Λνα		Dhe	Gln	
312	1113	Line	195	nrg	561	пец	Val	200	1113	цуз	1111	пор	205	OTII	THE	OIII	
	Glu	Leu		Glu	Leu	Ala	Glu		Ala	Arg	Leu	Gln		Gln	Leu	Asp	
316		210					215					220	_			•	
318	His	Arg	Gly	Asp	His	Pro	Leu	Thr	Pro	Gly	Ser	His	Tyr	Ala			
320						230					235						
				ON C													
				1: 37	72												
		2> TY			11			_									
				ISM: NCE:		o sag	orens	5									
				Asn		Ser	Ser	Thr	Asn	Ser	Ser	Val	T.e.11	Pro	Cvs	Pro	
333	1	пси	1114	11011	5	DCI	DCI	1111	71011	10	DCI	vui	LCu	110	15	110	
		Tyr	Arg	Pro	_	His	Arq	Leu	His		Val	Val	Tyr	Ser		Val	
337	-	-		20					25				-	30			
	Leu	Ala		Gly	Leu	Pro	Leu	Asn	Ala	Leu	Ala	Leu	Trp	Val	Phe	Leu	
341			35		_			40					45				
	Arg		Leu	Arg	Val	His		Val	Val	Ser	Val		Met	Cys	Asn	Leu	
345	7/1 ~	50	C^2	7 an	T 011	Ton	55 Pho	Th∽	T 011	802	T 033	60 Bro	17-1	7/ ~~ ~	T 011	Sor	
349	65	мта	Ser	Asp	теп	70	rne	1111	Leu	Ser	75	PIO	vaı	ALG	ьец	80	
		Tvr	Ala	Leu	His		Trp	Pro	Phe	Pro	-	Leu	Leu	Cvs	Gln		
353	- 3 -				85					90					95		
	Thr	Gly	Ala	Ile	Phe	Gln	Met	Asn	Met	Tyr	Gly	Ser	Cys	Ile	Phe	Leu	
357				100					105					110			
	Met	Leu		Asn	Val	Asp	Arg		Ala	Ala	Ile	Val		Pro	Leu	Arg	
361			115			_	_	120	_		_	_	125		_		
	Leu	_	His	Leu	Arg	Arg		Arg	Val	Ala	Arg		Leu	Cys	Leu	Gly	
365	TT - 1	130	77.	T	т1 -	T	135	Db -	7.1 -	77-7	D	140	71 -	7	17-1	11.2.	
	vai 145	ırp	нта	Leu	тте	150	۷dl	rne	нта	val	155	wra	HTG.	Arg	val	160	
		Pro	Ser	Arg	Cvs		Tur	Ara	Asn	Leu		Val	Ara	Len	Cvs	•	
373	* » L Y	110		**** 9	165	9	- y -	,, <u>r</u> A	1.5p	170	O L U	* 4.1		Leu	175		
	Glu	Ser	Phe	Ser		Glu	Leu	arT	Lvs		Ara	Leu	Leu	Pro		Val	
377				180				F	185	1	- 5			190			

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379 381	Leu	Leu	Ala 195	Glu	Ala	Leu	Gly	Phe 200	Leu	Leu	Pro	Leu	Ala 205	Ala	Val	Val
	Tyr	Ser 210		Gly	Arg	Val	Phe 215		Thr	Leu	Ala	Arg 220		Asp	Ala	Thr
	Gln 225	Ser	Gln	Arg	Arg	Arg 230	Lys	Thr	Val	Arg	Leu 235	Leu	Leu	Ala	Asn	Leu 240
391 393	Val	Ile	Phe	Leu	Leu 245	Cys	Phe	Val	Pro	Tyr 250	Asn	Ser	Thr	Leu	Ala 255	Val
397		_		260	Arg				265					270		
401	_	_	275	_	Gly			280					285		_	
405		290			Asp		295					300				
409	305		•		Arg	310					315					320
413				•	Thr 325		٠			330					335	
417				340	Ala				345					350		
421	_	Ser	355	_	Ser	птэ	Ser	360	Ser	Ser	rne	1111	365	Cys	FIO	GIII
425		370 370 Si			. 6											
							•									
430	<21	1> LF	ENGT	H: 1			•									
430 431	<21: <21:	1> LF 2> T	ENGTI YPE:	H: 1	46	o sam	oien:	5								
430 431 432	<213 <213 <213	1> LF 2> T	ENGTI YPE: RGANI	H: 14 PRT ISM:	46 Homo	o sap	oien:	5								
430 431 432 434	<213 <213 <213 <400	1> LE 2> TY 3> OE 0> SE	ENGTI YPE: RGANI EQUEI	H: 14 PRT ISM: NCE:	46 Homo	_			Glu	Gly 10	Ala	Ala	Ala	Leu	Gly 15	Gly
430 431 432 434 436 438 440 442	<21: <21: <21: <400 Met 1 Ala	1> LB 2> TY 3> OB 0> SB Trp Leu	ENGTI YPE: RGANI EQUEI Lys Phe	H: 14 PRT ISM: NCE: Leu Leu 20	Homo 6 Trp 5 Leu	Arg Leu	Ala Phe	Glu Ala	Leu 25	10 Gly	Val	Arg	Gln	Leu 30	15 Leu	Lys
430 431 432 434 436 438 440 442 444 446	<21: <21: <21: <400 Met 1 Ala	1> LH 2> TY 3> OH 0> SH Trp Leu	ENGTH YPE: RGANI EQUEN Lys Phe Arg 35	H: 10 PRT ISM: NCE: Leu Leu 20 Pro	Homo 6 Trp 5 Leu	Arg Leu Gly	Ala Phe Phe	Glu Ala Pro 40	Leu 25 Pro	10 Gly Gly	Val Pro	Arg Pro	Gln Gly 45	Leu 30 Leu	15 Leu Pro	Lys Phe
430 431 432 434 436 438 440 442 444 446 448 450	<21: <21: <400 Met 1 Ala Gln	1> LH 2> TY 3> OH 0> SH Trp Leu Arg Gly 50	ENGTH YPE: RGANI EQUEN Lys Phe Arg 35 Asn	PRT ISM: ISM: NCE: Leu 20 Pro	Homo 6 Trp 5 Leu Met	Arg Leu Gly Ser	Ala Phe Phe Leu 55	Glu Ala Pro 40 Ala	Leu 25 Pro Ala	10 Gly Gly Ser	Val Pro Ser	Arg Pro Glu 60	Gln Gly 45 Leu	Leu 30 Leu Pro	15 Leu Pro His	Lys Phe Val
430 431 432 434 436 438 440 442 444 446 448 450 452 454	<213 <213 <400 Met 1 Ala Gln Ile Tyr 65	1> LH 2> TY 3> OH 0> SH Trp Leu Arg Gly 50 Met	ENGTH YPE: RGANI EQUEN Lys Phe Arg 35 Asn	PRT PRT ISM: NCE: Leu 20 Pro Ile	Homo 6 Trp 5 Leu Met Tyr	Arg Leu Gly Ser Ser 70	Ala Phe Phe Leu 55 Gln	Glu Ala Pro 40 Ala Val	Leu 25 Pro Ala Tyr	10 Gly Gly Ser	Val Pro Ser Glu 75	Arg Pro Glu 60 Val	Gln Gly 45 Leu Gln	Leu 30 Leu Pro	15 Leu Pro His Arg	Lys Phe Val Arg
430 431 432 434 436 438 440 442 444 446 448 450 452 454 456 458	<21: <21: <400 Met 1 Ala Gln Ile Tyr 65 Ala	1> LH 2> TY 3> OH 0> SH Trp Leu Arg Gly 50 Met	ENGTH YPE: RGANI EQUEN Lys Phe Arg 35 Asn Arg	PRT ISM: ICE: Leu 20 Pro Ile Lys Arg	Homo 6 Trp 5 Leu Met Tyr Gln Glu 85	Arg Leu Gly Ser Ser 70 Gly	Ala Phe Phe Leu 55 Gln Arg	Glu Ala Pro 40 Ala Val Gln	Leu 25 Pro Ala Tyr Ala	10 Gly Gly Ser Gly Gly 90	Val Pro Ser Glu 75 Pro	Arg Pro Glu 60 Val	Gln Gly 45 Leu Gln Trp	Leu 30 Leu Pro Pro	15 Leu Pro His Arg Gly 95	Lys Phe Val Arg 80 Pro
430 431 432 434 436 438 440 442 444 446 450 452 454 456 458 460 462	<21: <21: <400 Met 1 Ala Gln Ile Tyr 65 Ala Ser	1> LH 2> TY 3> OH 0> SH Trp Leu Arg Gly 50 Met Pro	ENGTH YPE: RGANI EQUEN Lys Phe Arg 35 Asn Arg Gly Leu	PRT ISM: INCE: Leu 20 Pro Ile Lys Arg Asp 100	Homo 6 Trp 5 Leu Met Tyr Gln Glu 85 Leu	Arg Leu Gly Ser . Ser 70 Gly Trp	Ala Phe Phe Leu 55 Gln Arg	Glu Ala Pro 40 Ala Val Gln Pro	Leu 25 Pro Ala Tyr Ala Leu 105	10 Gly Gly Ser Gly Gly 90 Gly	Val Pro Ser Glu 75 Pro	Arg Pro Glu 60 Val Gly Leu	Gln Gly 45 Leu Gln Trp Val	Leu 30 Leu Pro Pro Gly 110	15 Leu Pro His Arg Gly 95 Thr	Lys Phe Val Arg 80 Pro Ser
430 431 432 434 436 438 440 442 444 446 450 452 454 460 462 464 467	<21: <21: <400 Met 1 Ala Gln Ile Tyr 65 Ala Ser Pro	1> LH 2> TY 3> OH 0> SH Trp Leu Arg Gly 50 Met Pro Trp	ENGTH YPE: RGANI RGANI EQUEN Lys Phe Arg 35 Asn Arg Gly Leu Ala 115	PRT ISM: INCE: Leu 20 Pro Ile Lys Arg Asp 100 Gly	Homo 6 Trp 5 Leu Met Tyr Gln Glu 85	Arg Leu Gly Ser . Ser 70 Gly Trp Pro	Ala Phe Phe Leu 55 Gln Arg Pro Leu	Glu Ala Pro 40 Ala Val Gln Pro Arg 120	Leu 25 Pro Ala Tyr Ala Leu 105 Asp	10 Gly Gly Ser Gly Gly 90 Gly Thr	Val Pro Ser Glu 75 Pro Arg	Arg Pro Glu 60 Val Gly Leu Phe	Gln Gly 45 Leu Gln Trp Val Pro 125	Leu 30 Leu Pro Pro Gly 110 Gly	15 Leu Pro His Arg Gly 95 Thr	Lys Phe Val Arg 80 Pro Ser Glu

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/019,114A

DATE: 03/29/2004

TIME: 09:56:28

Input Set : A:\3-19-04 KATO revised sequence listing.txt

Output Set: N:\CRF4\03292004\J019114A.raw

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date